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(12) **United States Patent**  
**Oefner et al.**(10) **Patent No.:** **US 6,929,911 B2**  
(45) **Date of Patent:** **Aug. 16, 2005**(54) **METHOD FOR DETERMINING GENETIC AFFILIATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN POPULATIONS**(75) Inventors: **Peter J. Oefner**, Redwood City, CA (US); **Peter A. Underhill**, Palo Alto, CA (US)(73) Assignee: **The Board of Trustees of the Leland Stanford Junior University**, Palo Alto, CA (US)

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(51) **Int. Cl.<sup>7</sup>** ..... **C12Q 1/68**; C12P 19/34; C07H 21/02; C07H 21/04(52) **U.S. Cl.** ..... **435/6**; 435/91.2; 536/23.5; 536/24.31; 536/24.33(58) **Field of Search** ..... 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.33(56) **References Cited**

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The present invention provides novel polymorphisms on the Y chromosome and methods of using these polymorphisms as well as known polymorphisms on the Y chromosome as indicators of evolutionary heritage. The polymorphisms of the present invention clustered to specific regions of the Y chromosome, and polymorphisms of particular use to the present methods are found in the non-recombining region of the human Y chromosome (NRY). These polymorphisms, including SNPs, insertions, and deletions, may be useful for numerous applications, including forensics, paternity testing, diagnosis and the like.

**40 Claims, 4 Drawing Sheets**